SPECIFICATION AMENDMENTS

(Insertions are indicated by bolded text; deletions are indicated by strike-through text)

Please delete the paragraphs at page 7, line 31, through page 8, line 14.

Please replace the paragraph beginning at page 22, line 23, with:

Alternately, peptides derived from the MART-1 protein sequence may modified to increase their immunogenicity by enhancing binding of the peptide to the MHC molecules in which the peptide is presented. Examples of such modified MART-1 peptides that may used are shown, but not limited to, the peptides in Table 14. In a preferred embodiment the MART-1 peptide that is modified to enhance its binding to MHC Class I molecules is AAGIGLTV (SEQ ID NO: 4). By way of example, the modified peptides ALGIGILTV **(SEQ ID NO: 50)** (M9-2-2L), WAGIGILTV **(SEQ ID NO: 53)** (M9-2-1W), FAGIGILTV **(SEQ ID NO: 54)** (M9-2-1F) and AAYIGILTV **(SEQ ID NO: 58)** (M9-2-3Y). The peptide or modified peptide may be conjugated to a carrier molecule to enhance the antigenicity of the peptide. Examples of carrier molecules, include, but are not limited to, human albumin, bovine albumin, lipoprotein and keyhole limpet hemo-cyanin ("Basic and Clinical Immunology" (1991) Stites, D.P. and Terr A.I. (eds) Appleton and Lange, Norwalk Connecticut, San Mateo, California).

Please replace the paragraph beginning at page 27, line 27, with:

By way of example, the HLA-A2 allele binds peptides of nine or ten amino acids. Examples of positions within the peptide that may be altered to enhance binding include, bur are not limited to, the first positions, the second position, the third position and the last position of the peptide. Any amino acid may be used to substitute or replace these positions within the immunogenic peptide sequence. For enhanced binding to HLA-A2 the amino acid at the second position of the peptide is preferably a hydrophobic aliphatic amino acid. Examples or amino acids that may be used at the second position include, but are not limited to, leucine, methionine, alanine, isoleucine, valine, threonine, or glycine. Preferably leucine or methionine is found at the second position of the peptide. The last amino acid of the peptide (either the 9th or 10th amino acid depending on the length of the peptide) is preferably a hydrophobic aliphatic amino acid. Examples of amino acids that may be used in the last position of the peptide include, but are not limited to, valine, methionine, leucine, alanine, isoleucine, threonine, or glycine. Preferably valine is found at the last position in the peptide. The amino acids at the first and third positions in the peptide may also be modified to enhance binding of the peptide to the MHC

Class I molecule. The amino acids at the first and third positions in the peptide may be any amino acid. Preferably, the amino acids at the first and third positions are hydrophobic aliphatic amino acids or aromatic amino acids. Examples of amino acids that maybe used at these positions include but are not limited to, leucine, methionine, valine, alanine, isoleucine, threonine, glycine, tryptophan, phenylalanine, tyrosine, serine, aspartic acid, or lysine. Examples of MA RT-1 peptides that may be modified include but are not limited to AAGIGILTV (SEQ ID NO: 4), EAAGIGLTV (SEQ ID NO: 17) and AAGIGILTVI (SEQ ID NO: 18) (peptides are presented in single letter amino acid code). By way of example the immunogenic MART-1 peptide AAGIGILTV (SEQ ID NO: 4) may be modified according to the following formula $X_1X_2X_3$IGILTX_4 **(SEQ ID NO: 122)** wherein

X_1 may be any amino acid, preferably any hydrophobic aliphatic amino acid, or aromatic amino acid. Examples of amino acids that may be used, but are not limited to, alanine, tryptophan, phenylalanine, tyrosine, lysine, isoleucine, leucine, methionine, threonine, glycine or serine.

X_2 may be any hydrophobic amino acid, preferably an aliphatic hydrophobic amino acids. Examples of amino acids that may be used include, but are not limited to leucine, methionine, isoleucine, valine, threonine, alanine or glycine.

Please replace the paragraph beginning at page 47, line 32, with:

By way of example modified gp100 peptides derived from the immunogenic gp100 peptide KTWGQYWQV (SEQ ID NO: 46) may have the formula $X_1X_2X_3$GQYWQX_4 **(SEQ ID NO: 123)** wherein:

X_1 may be any amino acid, preferably any hydrophobic aliphatic amino acid, or aromatic amino acid. Examples of amino acids that may be used include, but are not limited to, alanine, leucine, lysine, isoleucine, glycine, methionine, valine, threonine, tryptophan, phenylalanine, lysine or serine, aspartic acid or tyrosine;

X_2 may be any hydrophobic amino acid, preferably any aliphatic hydrophobic amino acid. Examples of amino acids that may be used include, but are not limited to, leucine, methionine, isoleucine, alanine, threonine, glycine, or valine. Most preferably leucine, methionine or isoleucine.

Please replace the paragraph beginning at page 48, line 23, with:

Examples of modified peptides are shown in Table 15. A preferred modified peptide is KIWGQYWQV **(SEQ ID NO: 70)** (G9-154-2I).

Please replace the paragraph beginning at page 48, line 25, with:

Alternately, the immunogenic gp100 ITDQVPFSV (G9-209; SEQ ID NO: 48) may be modified, such modification peptides may have the general formula $X_1X_2X_3QVPFSX_4$ **(SEQ ID NO:124)** wherein:

X_1 may be any amino acid, preferably any hydrophobic aliphatic amino acid, or aromatic amino acid. Examples of amino acids that may be used include, but are not limited to, leucine, methionine, alanine, isoleucine, valine, threonine, glycine, lysine, phenylalanine, tryptophan, or tyrosine, aspartic acid or serine;

X_2 may be any hydrophobic amino acid, preferably any aliphatic hydrophobic amino acid. Examples of amino acids that may be used include, but are not limited to, leucine, methionine, isoleucine, alanine, isoleucine, valine, or glycine;

X_3 may be any amino acid, preferably any hydrophobic aliphatic amino acid, or aromatic amino acid. Examples of amino acids that may be used include, but are not limited to, leucine, methionine, alanine, isoleucine, valine, threonine, glycine, lysine, phenylalanine, tryptophan, tyrosine, aspartic acid or serine; **and**

X_4 may be any hydrophobic amino acid, preferably any hydrophobic aliphatic amino acid. Examples of amino acids that may be used include, but are not limited to leucine, methionine, alanine, isoleucine, valine, or threonine~~;~~**.**

Please replace the paragraph beginning at page 49, line 22, with:

The modified peptides may have the general formula $X_1X_2X_3PGPVTX_4$ **(SEQ ID NO: 125)** wherein:

X_1 may be any amino acid, preferably any hydrophobic aliphatic amino acid, or aromatic amino acid. Examples of amino acids that may be used include, but are not limited to, leucine, methionine, alanine, isoleucine, valine, threonine, glycine, lysine, phenylalanine, tryptophan, or tyrosine, aspartic acid or serine;

X_2 may be any hydrophobic amino acid, preferably any aliphatic hydrophobic amino acid. Examples of amino acids that may be used include, but are not limited to, leucine, methionine, isoleucine, alanine, isoleucine, valine, or glycine;

X_3 may be any amino acid, preferably any hydrophobic aliphatic amino acid, or aromatic amino acid. Examples of amino acids that may be used include, but are not limited to, leucine, methionine, alanine, isoleucine, valine, threonine, glycine, lysine, phenylalanine, tryptophan, tyrosine, aspartic acid, or serine;

X_4 may be any hydrophobic amino acid, preferably any hydrophobic aliphatic amino acid. Examples of amino acids that may be used include, but are not limited to leucine, methionine, alanine, isoleucine, valine, threonine or glycine

Please replace the paragraph beginning at page 50, line 11, with:

Examples of modified peptides derived from YLEPGPVTA (G9-280; SEQ ID NO: 40) are shown in Table 17. A preferred modified peptide is YLEPGPVT **(SEQ ID NO: 127)** (G9-280-9V).

Please replace the paragraph beginning at page 57, line 22, with:

A cDNA library was constructed from poly A RNA from the HLA-A2$^+$ melanoma cell line, 501mel as described in (Miki, T., et al., (1989) Gene; 83:137-146 Miki et al. (1991) Proc. Nat. Acad. Sci. USA 88:5167-5171). Briefly, first strand cDNA was synthesized with a linker primer GGACAGGCCGATTGGTAA (T)$_{40}$ **(SEQ ID NO: 128)** followed by second strand cDNA synthesis. After treatment with T4 DNA ligase, an SfiI adaptor consisting of two oligonucleotides, CCAATCGCGACC **(SEQ ID NO: 43)** and GGTCGCGATTGGTAA **(SEQ ID NO: 44)** was ligated to the end of the cDNA. The cDNA was digested with SfiI and the digested fragment was isolated by passing through a spun column. The cDNA was then mixed with bacteriophage λpCEV27 (Miki, T. et al., (1991) Proc. Natl. Acad. Science (USA) 88: 5167-5771 vector arms prepared by SfiI digestion and in vitro packaging was performed.

Please replace the paragraph beginning at page 60, line 26, with:

A cDNA library from the HLA-A2$^+$ 501mel melanoma cell line was transfected into two highly transfectable HLA-A2.1$^+$ cancer cell lines, MDA231 and A375. These cell lines were not lysed by melanoma specific TIL but were lysed by HLA-A2 restricted influenza M1 specific CTL after incubation with the M1$_{58\text{-}66}$ peptide (GILGFVFTL; **(SEQ ID NO: 45)** single letter code) derived the influenze matrix protein or infection with a recombinant vaccinia virus containing the M1 gene (data not shown). Thus, these cells lines exhibited normal antigen processing and presenting ability but were not lysed by these melanoma specific TIL because of lack of expression of the relevant melanoma antigens. After selection with G418, approximately 6700 transfected clones from each cell line were isolated and rescreened. Of these closed, eight MDA231 and seven A375 clones were positive in a second screening assay.

Please replace the Table 5 on page 73 with:

Table 5. Lysis of T2 cells preincubated with synthetic MART-1 peptides

Target	Peptide		A42	TIL 1235	TIL 660	TIL 1074
			% specific lysis			
501mel	none		47	30	31	41
397mel	none		1	0	1	2
T2	none		-2	-3	-1	1
T2	M9-1	TTAEEAAGI **(SEQ ID NO: 3)**	-10	-5	-5	-4
T2	M9-2	AAGIGILTV **(SEQ ID NO: 4)**	64	80	40	56
T2	M9-3	GIGILTVIL **(SEQ ID NO: 5)**	18	20	0	10
T2	M9-4	GILTVILGV **(SEQ ID NO: 6)**	1	-1	-3	2
T2	M9-5	ILTVILGVL **(SEQ ID NO: 7)**	-2	-1	-5	-1
T2	M9-6	LTVILGVLL **(SEQ ID NO: 8)**	1	0	1	0
T2	M9-7	TVILGVLLL **(SEQ ID NO: 9)**	-2	-3	-2	1
T2	M9-8	VILGVLLLI **(SEQ ID NO: 10)**	1	5	-2	-2
T2	M9-9	ALMDKSLHV **(SEQ ID NO: 11)**	-1	-4	-8	0
T2	M9-10	SLHVGTQCA **(SEQ ID NO: 12)**	-1	1	-8	4
T2	M9-11	PVVPNAPPA **(SEQ ID NO: 13)**	-2	0	4	-1
T2	M9-12	NAPPAYEKL **(SEQ ID NO: 14)**	1	-2	0	6
T2	M10-1	YTTAEEAAGI **(SEQ ID NO: 15)**	-4	-2	-3	3
T2	M10-2	TAEEAAGIGI **(SEQ ID NO: 16)**	7	11	12	15
T2	M10-3	EAAGIGILTV **(SEQ ID NO: 17)**	55	66	31	51
T2	M10-4	AAGIGILTVI **(SEQ ID NO: 18)**	34	68	29	21
T2	M10-5	GILTVILGVL **(SEQ ID NO: 19)**	-1	2	7	10
T2	M10-6	ILTVILGVLL **(SEQ ID NO: 20)**	1	6	6	7
T2	M10-7	LTVILGVLLL **(SEQ ID NO: 21)**	-2	-1	-1	2
T2	M10-8	TVILGVLLLI **(SEQ ID NO: 22)**	-6	-1	-1	11
T2	M10-9	RALMDKSLHV **(SEQ ID NO: 23)**	3	5	8	11
T2	M10-10	SLHVGTQCAL **(SEQ ID NO: 24)**	-2	-8	2	9
T2	M10-11	SLQEKNCEPV **(SEQ ID NO: 25)**	3	2	2	9

Twenty-three peptides (12 9-mers and 11 10-mers) (<90% purity) were synthesized and the lysability by TIL clone A42, TIL lines TIL1235, TIL660, and TIL1074 derived from different patients was tested against HLA-A2$^+$ T2 cells preincubated with each peptide (10ug/ml) in a

4h-^{51} Cr release cytotoxicity assay at E:T ration of 20:1 for A42 and 40:1 for other TIL lines. T2 cells were lysed will when incubated with M9-2, M10-3 and M10-4. M10-3 and M10-4 contain the entire M9-2 sequence (underlined).

Please replace the Table 10 on page 89 with:

Table 10. TIL1200 Lysis of the T2 HLA-A2^{+} Cell Line Pulsed with the Peptide, LLDGTATLRL **(SEQ ID NO: 33)**

Target	HLA-A2	Peptide*	TIL1200	TIL1235^{+}
		(ug/ml)	(% Specific lysis)$^{++}$	
501mel	+	0	66	51
397mel	-	0	1	0
T2	+	0	2	1
T2	+	40	28	ND^{++}
T2	+	10	32	0
T2	+	1	24	ND
T2	+	0.1	6	ND
T2	+	0.01	0	ND
T2	+	0.001	2	ND

*TIL1200 lysed T2 cells pulsed with the 10-mer peptide, LLDGTATLRL **(SEQ ID NO: 33)** (457-466), but not other 29 peptide SEQ ID NO: 27 (residues 273-281, 297-306, 373-381, 399-407, 399-408, 409-418, 456-464, 463-471, 465-473, 476-485, 511-520, 519-528, 544-552, 544-553, 570-579, 576-584, 576-585, 585-593, 592-600, 597-605, 597-606, 602-610, 602-611, 603-611, 605-614, 606-614, 606-615, 619-627, 629-638)

$^{+}$TIL1235 is an HLA-A2 restricted melanoma specific CTL that does not recognize gp100.

**E:T of 50:1

$^{++}$ND, not done.

Please replace the paragraph beginning at page 92, line 22, with:

Peptides were a synthesized by a solid phase method using a peptide synthesizer (model AMS 422; Gilson Co. Inc., Worthington, OH) (>90% purity). The peptides to be synthesized were selected from the reported human sequence of gp100 based on HLA-A2.1 binding motifs

(Falk, K., (1991) *Nature* 351:290; Hunt, D. F., et al, (1992) *Science* 225:1261; Ruppert, J., et al. (1993) *Cell* 74:929; Kubo, RT, et al. (1994) *J Immunol.* 152:3913). The following peptides were tested: Eight 8-mer peptides (with residues starting at –199, 212, 218, 237, 266, 267, 268, 269; ~~see Figure 7A~~), eighty-four 9-mer peptides with residues starting at - 2, 4, 11, 18, 154, 162, 169, 171, 178, 199, 205, 209, 216, 241, 248, 250, 255, 262, 266, 267, 268, 273, 278, 280, 273, 286, 287, 298, 290, 309, 316, 332, 335, 350, 354, 358, 361, 371, 373, 384, 389, 397, 399, 400, 402, 407, 408, 420, 423, 425, 446, 449, 450, 456, 463, 465, 485, 488, 501, 512, 531, 544, 563, 570, 571, 576, 577, 578, 583, 585, 590, 592, 595, 598, 599, 601, 602, 603, 604, 606, 607, 613, 619, 648, ~~see Figure 7A~~) and seventy-seven, 10-mer peptides with residues starting at – 9, 17, 57, 87, 96, 154, 161, 169, 177, 197, 199, 200, 208, 216, 224, 232, 240, 243, 250, 266, 267, 268, 272, 285, 287, 289, 297, 318, 323, 331, 342, 350, 355, 357, 365, 380, 383, 388, 391, 395, 399, 400, 406, 407, 409, 415, 432, 449, 453, 457, 462, 476, 484, 489, 492, 511, 519, 536, 543, 544, 548, 568, 570, 571, 576, 577, 584, 590, 595, 598, 599, 601, 602, 603, 605, 611, 629; ~~see Figure 7A~~) were synthesized. Possible epitopes identified in the first screening were further purified by HPLC on a C-4 column (VYDAC, Hesperia, CA) (>98% purity) and the molecular weights of the peptides were verified by mass spectrometry measurement as previously described (Example 3: Kawakami, Y., et al., (1994) J. Exp. Med. 180:347; Kawakami, Y., et al., (1994) *Proc Natl Acad Sci* (*USA*) 91:6458).

Please replace the paragraph beginning at page 93, line 24, with:

Soluble HLA-A2.1 heavy chain, human beta 2-microglobulin, radiolabeled peptide HBC_{18-27} (FLPSDYFPSV **(SEQ ID NO: 126)**) and various concentrations of the sample peptides were coincubated in the presence of protease inhibitors for 2 days at room temperature as previously desctibed (Ruppert, J., et al., (1993) Cell 74:929; Kubo, RT, et la., (1994), J. Immunol. 152:3913; Sett A., et al., (1994). Molecular Immunol. 31:813). The percentage of labeled peptide bound to HLA-A2.1 was calculated after separation by gel filtation and the concentration of the sample peptide necessary to inhibit 50% of the binding of the labeled peptide was calculated. The relative affinity of peptidesto HLA-A2.1 were also calculated as a ration (concentration of the standard HBc_{18-27} peptide to inhibit 50% of the binding of the labeled peptide/concentration of the sample peptide to inhibit 50% of the binding of the labeled peptide) as previously described (Sett A., et al., (1994) Molecular Immunol. 31:813). Peptide binding was defined as high (50% inhibition at ,50nM ration .0.1), intermediate (50-50nM ration 0.1-0.01) or weak (.500nM, ration ,0.01) (Ruppert, J., et al., (1993) Cell 74:929; Kubo, RT, et al., (1994) J. Immunol. 152:3913; Sett A., et al., (1994) Molecular Immunol 31:813).

Please replace the paragraph beginning at page 96, line 32, with:

To complement the epitope identification using the known HLA-A2.1 binding motifs, another method was also used to identify regions possible containing epitopes. Five gp100 cDNA fragments, 4 generated by exonuclease deletion from the 3' –end of the cDNA (D3, D4, D5, C4) as well as a partial cDNA clone lacking the first 705 base pairs of the 5' –coding region (25TR), were inserted into the pcDNA3 plasmid and transfected into COS7 cells along with the HLA-A2.1 cDNA. ~~The locations of the fragments are shown in Figure 7a.~~ The recognition of these transfectants by the 4 gp100 reactive TIL was evaluated using an IFN-γ release assay ~~(Figure 7B)~~. TIL1200 recognized COS cells transfected with the fragments, 25TR, D5, D4, or C4, but not with D3, suggesting that at least 2 epitopes existed in the regions of amino acid residues 146-163 and 236-661. $G9_{154}$ and $G10_{154}$ were the only peptides which contained HLA-A2.1 binding motifs in the region 146-163 and both were recognized by TIL1200. G10-4 was located in the region 236-661 and was recognized by TIL1200. TIL620-1 recognized COS cells transfected with C4 but not with D3, D5, D4 or 25TR, suggesting that the epitope existed within residues 187-270. $G9_{209}$ and $G10_{208}$ which were recognized by TIL620-1, were located in this region. TIL620-2 another subculture of TIL620, also recognized COS cells transfected with D5 and D4, but not D3, and recognized $G9_{154}$ and $G10_{154}$ in the region 147-163, also recognized by TIL1200. TIL660-1 and TIL1143 recognized COS cells transfected with C4 or 25TR, but not with D3, D5, or D4, suggesting that epitopes existed in the 2 regions 187-270 and 236-661. $G9_{280}$ located in the fragment 25TR, but not in the fragment C4, was recognized by TIL660 and TIL1143.

Please replace the paragraph beginning at page 97, line 31, with:

With the exception of G10-4, which required a concentration of 1ug/ml to sensitize T2 cells for CTL lysis (Example 3; Kawakami, Y., et al., (1994) _Proc Natl Acad Sci_ (USA) 91:6458), all gp100 epitopes identified in this study could sensitize T2 cells for CTL lysis at a concentration of 1ng/ml ~~(Figures 8A-8D)~~. G10-5 appeared to be inhibitory to the cytotoxic activity of CTL at concentration greater than 10ng/ml since lysis of T2 cells incubated with G10-5 at more than 10ng/ml was repeatedly lower than at 1-10ng/ml in this assay condition in which the peptide was present in the medium during entire 4h cytotoxicity assay ~~(Figure 8D)~~. The relative binding affinity of these epitopes to HLA-A2.1 was also measured using an in vitro competitive binding assay (Table 13). ~~$G9_{154}$ and (1010nM) which contains an extra leucine at~~

~~the C terminus of~~ G9$_{154}$, had an higher binding affinity (50% inhibition of the standard peptide at 11nM) to the HLA-A2.1 molecule than G10$_{154}$ (1010nM)
and could sensitize T2 cells at lower concentration than G10$_{154}$ ~~(Figure 8A)~~. G9$_{209}$ also bound to HLA-A2.1 with higher affinity (84nm) than G10$_{208}$ (2080nM), which contains an extra threonine at the N-terminus, and could sensitize T2 cells at lower concentrations of peptide than G10$_{208}$ ~~(Figure 8B)~~. Thus, the 9-mer peptides were superior to the corresponding 10 mer peptides in the sensitization of T2 cells to CTL lysis, and they also had higher binding affinities to HLA-A2.1. This was also the case for the identified MART-1 9 and 10 amino acid peptides (M9-2, M10-3, M10-4) (Example 2; Kawakami, Y., et al., (1994). *J. Exp. Med.* 180:347). The results of the peptide titration in the T2 cell lysis assay correlated with the results of the HLA-A2.1 binding affinity as measured by the in vitro binding assay. The other gp100 epitopes, G9$_{280}$, and G10-4 or G10-5 had binding affinities for HLA-A2.1 with 50% inhibition at 95nM, 483nM, or 13nM, respectively. The HLA-A2.1 binding affinities of the previously identified HLA-A2 restricted melanoma epitopes in MART-1 (Example 2; Kawakami, Y., et al., (1994) *J. Exp. Med.* 180:347) and tyrosinase (Wolfel, T., (1994) *Eur J. Immunol.* 24:759) were also measured (M9-2 (397nM), M10-3 (2272nM), M10-4 (5555nM), T9, (333nM), T9$_{369}$ (40nM)). Except for the 10mer peptides (G10$_{154}$, G10$_{208}$, GM10-3, GM10-4), for which overlapping 9-mer epitopes (G9$_{154}$, G9$_{209}$, M9-2) existed, all melanoma epitopes had either high (G9$_{154}$, G10-5, T9$_{369}$) or intermediate (G9$_{209}$, G9$_{280}$, G10-4, M9-2, T9$_{1}$) binding affinities to HLA-A2.1.

Please replace the paragraph beginning at the end of Table 12 on page 101, with:

Lysis by TIL of T2 cells preincubated with MART1 epitope, M9-2 (AAGIGILTV **(SEQ ID NO: 4)**) and gp100 epitopes, G9$_{154}$ (KTWGQYWQV **(SEQ ID NO: 46)**), G10$_{156}$ (KTWGQYWQVL **(SEQ ID NO: 47)**), G9$_{209}$ (ITDQVPFSV **(SEQ ID NO: 48)**), G10$_{208}$ (TITDQVPFSV **(SEQ ID NO: 49)**), G9$_{280}$ (YLEPGPVTA **(SEQ ID NO: 40)**), G10-4 (LLDGTATLRL **(SEQ ID NO: 33)**)< G10-5 (VLYRYGSFSV **(SEQ ID NO: 34)**) at 1ug/ml (* 1ng.ml), was measured by 4h- ^{51}Cr release assays. TIL which was administered into the autologous patient, but were separately cultured. 624mel, HLA-A2+ gp100+, MART 1+ melanoma cell line, 397mel, HLA-A2- melanoma cell line. T2cells, HLA-A2+ T cell-B-cell hybridoma. Bold: statistically significant lysis

Please replace Table 13 on page 102 with:

Table 13. The relative binding affinity of the human melanoma epitopes to HLA-A2.1

Protein	Peptide (nM)	Sequence Standard [b]	50% inhibition	Ration to
Gp100	G9$_{1J4}$	KTWGQYWQV **(SEQ ID NO: 46)**	11	0.45
	G10$_{1J4}$	KTWGQYWQVL **(SEQ ID NO: 47)**	1010	0.005
	G9$_{:09}$	ITDQVPFSV **(SEQ ID NO: 48)**	84	0.06
	G10$_{208}$	TITDQVPFSV **(SEQ ID NO: 49)**	2080	0.0024
	G9$_{280}$	YLEPGPVTA **(SEQ ID NO: 40)**	95	0.053
	G10-4	LLDGTATLRL **(SEQ ID NO: 33)**	483	0.01
	G10-5	VLYRYGSFSV **(SEQ ID NO: 34)**	13	0.38
MART-1	MB-2	AAGIGILTV **(SEQ ID NO: 4)**	395	0.013
	M10-3	EAAGIGILTV **(SEQ ID NO: 17)**	2272	0.0022
	M10-4	AAGIGILTVI **(SEQ ID NO: 18)**	5555	0.0009
Tyrosinase	T9,	MLLAVLYCL **(SEQ ID NO: 31)**	333	0.015
	T9$_{369}$	YMNGTMSQV **(SEQ ID NO: 32)**	40	0.13.

[a]Concentration of sample peptide required for 50% inhibition of the standard radiolabeled peptide HBC18-27. [b]Ratio of the binding affinity of the sample peptide to that of the standard peptide (50% inhibition at 5nM). Peptides are defined as high (50% inhibition at <50nM, ratio .0.1), intermediate (50-500nM, ration 0.1 0.01) and weak (>500nM, ratio,0.01) binding peptides.

Please replace the paragraph beginning at page 103, line 6, with:

Peptides were synthesized by a solid phase method using a multiple peptide synthesizer and purified by HPLC, as previously described (Rivoltini, L et al., (1995) Journal of Immunology Volume 154: 2257-2265). The relative binding of peptides to HLA-A2.1, based on the inhibition of binding of a radiolabeled standard peptide to detergent-solubilized MHC molecules, was performed as previously described (Rivoltini, L. et al., (1995) Journal of Immunology Volume 154:2257-2265). Briefly, various doses of the test peptides (ranging from 100 μM to 1nM) were coincubated together with the 5nM radiolabeled Hbc 18-27 (FLPSDYFPSV **(SEQ ID NO: 126)**) peptide and HLA-A2.1 heavy chain and β2-microglobulin for 2 days at room temperature in the presence of protease inhibitors. The percentage of MHC-bound radioactivity was determined by gel filtration and the 50% inhibitory dose was calculated for each peptide.

Please replace Table 14 on page 107 with:

Table 14 Modified MART-1 M9-2 peptides

Peptide	Sequence	Binding Affinity to HLA-A2.1 (nM)	Recognition by M9-2 reactive T-cell
M9-2 parent	AAGIGILTV **(SEQ ID NO: 4)**	1064	+
M9-2-2L	ALGIGILTV **(SEQ ID NO: 50)**	10	+
M9-2-2M	AMGIGILTV **(SEQ ID NO: 51)**	14	-
M9-2-2I	AIGIGILTV **(SEQ ID NO: 52)**	77	-
M9-2-1W	WAGIGILTV **(SEQ ID NO: 53)**	1351	+
M9-2-1F	FAGIGILTV **(SEQ ID NO: 54)**	244	+
M9-2-1Y	YAGIGILTV **(SEQ ID NO: 55)**	136	-
M9-2-3W	AAWIGILTV **(SEQ ID NO: 56)**	65	-
M9-2-3F	AAFIGILTV **(SEQ ID NO: 57)**	67	-
M9-2-3Y	AAYIGILTV **(SEQ ID NO: 58)**	102	+
M9-2-1K2L	KLGIGILTV **(SEQ ID NO: 59)**	14	-
M9-2-1K2M	KMGIGILTV **(SEQ ID NO: 60)**	27	-
M9-2-1K2I	KIGIGILTV **(SEQ ID NO: 61)**	94	-
M9-2-1W2L	WLGIGILTV **(SEQ ID NO: 62)**	11	-
M9-2-1F2L	FLGIGILTV **(SEQ ID NO: 63)**	1.8	-
M9-2-1Y2L	YLGIGILTV **(SEQ ID NO: 64)**	3.2	-
M9-2-2L3W	ALWIGILTV **(SEQ ID NO: 65)**	5.5	-
M9-2-2L3F	ALFIGILTV **(SEQ ID NO: 66)**	1.4	-
M9-2-2L3Y	ALYIGILTV **(SEQ ID NO: 67)**	3.7	-

Please replace Table 15 on page 108, with:

Table 15 Modified gp100 G9-154 peptides

Peptide	Sequence	Binding Affinity to HLA-A2.1 (nM)	Recognition by G9-154 reactive T-cell
G9-154-parent	KTWGQYWQV **(SEQ ID NO: 46)**	5.7	+
G9-154-2L	KLWGQYWQV **(SEQ ID NO: 68)**	2	+
G9-154-2M	KmWGQYWQV **(SEQ ID NO: 69)**	6.5	+
G9-154-2I	KIWGQYWQV **(SEQ ID NO: 70)**	3	+
G9-154-1W	WTWGQYWQV **(SEQ ID NO: 71)**	60	-
G9-154-1F	FTWGQYWQV **(SEQ ID NO: 72)**	1.6	-
G9-154-1Y	YTWGQYWQV **(SEQ ID NO: 73)**	2.5	-
G9-154-1A	ATWGQYWQV **(SEQ ID NO: 74)**	5.2	+
G9-154-1L	LTWGQYWQV **(SEQ ID NO: 75)**	3.4	+
G9-154-3Y	KTYGQYWQV **(SEQ ID NO: 76)**	30	+
G9-154-3F	KTFGQYWQV **(SEQ ID NO: 77)**	21	+
G9-154-1A2L	ALWGQYWQV **(SEQ ID NO: 78)**	2.3	+
G9-154-1L2L	LLWGQYWQV **(SEQ ID NO: 79)**	1.6	+
G9-154-1W2L	WLWGQYWQV **(SEQ ID NO: 80)**	2.8	-
G9-154-1F2L	FLWGQYWQV **(SEQ ID NO: 81)**	2.6	-
G9-154-1Y2L	YLWGQYWQV **(SEQ ID NO: 82)**	1.7	-

Please replace Table 16 on page 109, with:

Table 16. Modified gp100 G9-209 peptides

Peptide	Sequence	Binding Affinity to HLA-A2.1 (nM)	Recognition by G9-209 reactive T-cell
G9-209 parent	ITDQVPFSV **(SEQ ID NO: 48)**	172	+
G9-209-2L	ILDQVPFSV **(SEQ ID NO: 83)**	3.3	+
G9-209-2M	IMDQVPFSV **(SEQ ID NO: 84)**	19	+
G9-209-2I	IIDQVPFSV **(SEQ ID NO: 85)**	40	+
G9-209-1F	FTDQVPFSV **(SEQ ID NO: 86)**	61	+
G9-209-1W	WTDQVPFSV **(SEQ ID NO: 87)**	711	+
G9-209-1Y	YTDQVPFSV **(SEQ ID NO: 88)**	85	+
G9-209-3W	ITWQVPFSV **(SEQ ID NO: 89)**	34	-
G9-209-3F	ITFQVPFSV **(SEQ ID NO: 90)**	66	-
G9-209-3Y	ITYQVPFSV **(SEQ ID NO: 91)**	33	-
G9-209-3A	ITAQVPFSV **(SEQ ID NO: 92)**	95	-
G9-209-3M	ITMQVPFSV **(SEQ ID NO: 93)**	40	-
G9-209-3S	ITSQVPFSV **(SEQ ID NO: 94)**	649	-
G9-209-2L3W	ILWQVPFSV **(SEQ ID NO: 95)**	1.7	-
G9-209-2L3F	ILFQVPFSV **(SEQ ID NO: 96)**	2	-
G9-209-2L3Y	ILYQVPFSV **(SEQ ID NO: 97)**	5	-
G9-209-2L3A	ILAQVPFSV **(SEQ ID NO: 98)**	11	-
G9-209-2L3M	ILMQVPFSV **(SEQ ID NO: 99)**	7.6	-
G9-209-2L3S	ILSQVPFSV **(SEQ ID NO: 100)**	20	-
G9-209-1W2L	WLDQVPFSV **(SEQ ID NO: 101)**	12	+
G9-209-1F2L	FLDQVPFSV **(SEQ ID NO: 102)**	2.2	+
G9-209-1Y2L	YLDQVPFSV **(SEQ ID NO: 103)**	2.3	+

[a] Concentration of sample peptide required for 50% inhibition of the standard radiolabeled peptide HBC18-27. Peptides are defined as high (50% inhibition at <50nM), intermediate (50-500nM) and weak (>500nM) binding peptides. (see ref gp100 epitope)

Please replace Table 17 on page 110 with:

Table 17 Modified gp100 G9-209 peptides

Peptide	Sequence	Binding Affinity to HLA-A2.1 (nM)	Recognition by G9-209 reactive T-cell
G9-280 parent	YLEPGPVTA **(SEQ ID NO. 40)**	455	+
G9-280-9V	YLEPGPVTV **(SEQ ID NO:104)**	48	+
G9-280-9L	YLEPGPVTL **(SEQ ID NO:105)**	88	+
G9-280-9I	YLEPGPVTI **(SEQ ID NO:106)**	65	+
G9-280-1F	FLEPGPVTA **(SEQ ID NO:107)**	125	+
G9-280-1W	WLEPGPVTA **(SEQ ID NO:108)**	833	+
G9-280-3Y	YLYPGPVTA **(SEQ ID NO:109)**	17	-
G9-280-3W	YLWPGPVTA **(SEQ ID NO:110)**	3.2	-
G9-280-3F	YLFPGPVTA **(SEQ ID NO:111)**	3.2	-
G9-280-3M	YLMPGPVTA **(SEQ ID NO:112)**	4.3	-
G9-280-3S	YLSPGPVTA **(SEQ ID NO:113)**	42	-
G9-280-3A	YLAPGPVTA **(SEQ ID NO:114)**	9.3	-
G9-280-3M9V	YLMPGPVTV **(SEQ ID NO:115)**	12	-
G9-280-3S9V	YLSPGPVTV **(SEQ ID NO:116)**	23	-
G9-280-3A9V	YLAPGPVTV **(SEQ ID NO:117)**	15	-
G9-280-3Y9V	YLYPGPVTV **(SEQ ID NO:118)**	8.9	-
G9-280-3F9V	YLFPGPVTV **(SEQ ID NO:119)**	5.8	-
G9-280-3W9V	YLWPGPVTV **(SEQ ID NO:120)**	7.4	-

Please replace the paragraph beginning at page 115, line 5, with:

T-lymphocytes presensitized to the melanoma antigen may be effective in therapeutically treating mammals afflicted with melanoma. The T-lymphocytes will be isolated from peripheral blood lymphocytes or tumor infiltrating lymphocytes and exposed in vitro to the MART-1 protein or peptide. T-lymphocytes are isolated from peripheral blood or melanoma tumor suspensions and cultured in vitro (Kawakami, Y et al., (1988) J. Exp. Med. 168: 2183-2191). The T-lymphocytes are exposed to the MART-1 peptide AAGIGILTV **(SEQ ID NO: 4)** for a period of about 1-16 hours at a concentration of about 1 to about 10mg/ml. T-lymphocytes exposed to the antigen will be administered to the mammal, preferably a human at about 10^9 to about 10^{12} lymphocytes may be administered either intravenously, intraperitoneally or intralesionally. This treatment may be administered concurrently with other therapeutic treatments such as cytokines, radiotherapy, surgical exicision of melanoma lesions and chemotherapeutic drugs, adoptive T lymphocyte therapy. Alternatively, the T-lymphocytes may be exposed to the gp100 immunogenic peptides or modified immunogenic peptides describes herein.